

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/552,857
Source: P4/10
Date Processed by STIC: 10/24/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/24/2005

PATENT APPLICATION: US/10/552,857

TIME: 10:50:34

Input Set : A:\sequence.txt

Output Set: N:\CRF4\10242005\J552857.raw

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4 <110> APPLICANT: Agriculture Victoria Services Pty Ltd
5     AgResearch Limited
6     Spangenberg, German
7     Emmerling, Michael
8     Simmonds, Jason
9     Winkworth, Amanda
10    Panter, Stephen
12 <120> TITLE OF INVENTION: Chlacone synthase dihydroflavonol-4-reductase and
13     leucoanthrocyanidine reductase for clover, medic
14     rygrass or fescue
17 <130> FILE REFERENCE: FREE.P-007
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/552,857
C--> 20 <141> CURRENT FILING DATE: 2005-10-14
20 <150> PRIOR APPLICATION NUMBER: 2003901797
21 <151> PRIOR FILING DATE: 2003-04-14
24 <150> PRIOR APPLICATION NUMBER: 2003904369
25 <151> PRIOR FILING DATE: 2003-08-14
28 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/00494
W--> 29 <151> PRIOR FILING DATE: 2004-4-14
32 <160> NUMBER OF SEQ ID NOS: 77
35 <170> SOFTWARE: PatentIn version 3.2
38 <210> SEQ ID NO: 1
39 <211> LENGTH: 1447
40 <212> TYPE: DNA
41 <213> ORGANISM: Trifolium repens
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48 acgcatatta tatatatata tatatagtct ataattgaaa gaaactgcta aagatattat      120
51 taagatatgg tgagtgtagc tgaaattcgc aaggctcaga gggctgaagg ccctgcaacc      180
54 attttggccca ttggcactgc aaatccacca aaccgtgttg agcagagcac atatcctgat      240
57 ttctacttca aaattacaaa cagtgagcac aagactgagc tcaaagagaa gttccaacgc      300
60 atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga gattttgaaa      360
63 gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca agacatggtg      420
66 gtggttgagg tacctagact tgggaaggag gctgcagtca aggccattaa agaatggggt      480
69 caaccaaagt caaagattac tcaacttaatc ttttgcacca caagtgggtg tgacatgcct      540
72 ggtgctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa aaggatatatg      600
75 atgtaccaac aaggttggtt tgcaggaggc acggtgcttc gtttggcaaa agatttggcc      660
78 gagaacaaca aaggtgctcg tgtgctagtt gtttgttctg aagtcaccgc agtcacattt      720
81 cgcggcccca gtgatactca cttggacagt cttgttggac aagcattggt tggagatgga      780
84 gccgctgcac taattgttgg ttctgatcca gtgcctgaaa ttgagaaacc aatatttgag      840
87 atggtttgga ctgcacaaac aattgctcca gacagtgaag gtgccattga tggatcatctt      900
90 cgtgaagctg ggctaacatt tcatcttctt aaagatgttc ctgggattgt atcaaagaac      960
93 attaataaag cattggttga ggctttccaa ccattaggaa tttctgacta caactcaatc      1020

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99 ttgaagcccg aaaagatgag ggccacgagg gaagttctaa gtgaatatgg aaacatgtca 1140
102 agcgcattgt tattgttcat cttagatgag atgcggaaga aatcggctca aaatggactt 1200
105 aagacaactg gagaaggact tgattggggg gtgttggtcg gcttcggacc aggacttacc 1260
108 attgaaaccg ttgttcttcg tagcgtggct atataagatg tgtgattggt tttattttaa 1320
111 tgtattactt ttaatcttgc tgccttgaat ttcgatttaa gaataaataa atatatcttt 1380
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117 cgaattc 1447
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122 <211> LENGTH: 389
123 <212> TYPE: PRT
124 <213> ORGANISM: Trifolium repens
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131 1 5 10 15
135 Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Pro Asn Arg Val Glu
136 20 25 30
140 Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
141 35 40 45
145 Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
146 50 55 60
150 Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
151 65 70 75 80
155 Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
156 85 90 95
160 Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
161 100 105 110
165 Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
166 115 120 125
170 Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
171 130 135 140
175 Thr Lys Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr
176 145 150 155 160
180 Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
181 165 170 175
185 Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
186 180 185 190
190 Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
191 195 200 205
195 Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
196 210 215 220
200 Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
201 225 230 235 240
205 Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
206 245 250 255
210 His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
211 260 265 270
215 Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln
216 275 280 285

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220 Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
 221 290 295 300
 225 Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Gln Lys Leu Ala Leu Lys
 226 305 310 315 320
 230 Pro Glu Lys Met Arg Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn
 231 325 330 335
 235 Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
 236 340 345 350
 240 Ser Ala Gln Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
 241 355 360 365
 245 Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
 246 370 375 380
 250 Arg Ser Val Ala Ile
 251 385

255 <210> SEQ ID NO: 3

256 <211> LENGTH: 2394

257 <212> TYPE: DNA

258 <213> ORGANISM: Trifolium repens

261 <400> SEQUENCE: 3

262 gaattcgatt aagcagtggt aacaacgcag agtacgcggg gattcaatct gttgtgcata 60
 265 aaattcactc attgcataga aaaccatata catttgatct tgcaaagaag aaatatggga 120
 268 gacgaaggta tagtgagagg tgtcacaaag cagacaaccc ctgggaaggc tactatatgt 180
 271 gctcttggca aggcattccc tcaccaactt gtgatgcaag agtggttagt tgatggttat 240
 274 tttaggggaca ctaattgtga caatcctgaa cttaagcaga aacttgctag actttgtaag 300
 277 acaaccacgg taaaaacaag gtatgttggt atgaatgagg agatactaaa gaaatatcca 360
 280 gaacttggtt tgcgaaggcg ctcaactgta aaacaacgtt tagagatatg taatgaggca 420
 283 gtaacacaaa tggcaattga agcttcccaa gtttgccaa agaattgggg tagatcctta 480
 286 tcggacataa ctcatgtggt ttatgtttca tctagtgaag ctagattacc cgggtggtgac 540
 289 ctatacttgt caaaaggact aggactaaac cctaaaattc aaagaaccat gctctatttc 600
 292 tctggatgct cgggaggcgt agccggcctt cgcgttgcca aagacgtagc tgagaacaac 660
 295 cctggaagta gagttttgct tgcacttcg gaaactacaa ttattggatt caagccacca 720
 298 agtggtgata gaccttatga tcttggttgg gtggcactct ttggagatgg tgctggtgca 780
 301 atgataattg gctcagaccc ggtatttgaa actgagacac cattgtttga gctgcatact 840
 304 tcagctcagg agttttatac agacaccgag aagaaaattg atgggcggct gacggaggag 900
 307 ggcataagtt tcacactagc aagggaaact ccgcagataa tcgaagacaa tgttgaggga 960
 310 ttctgtaata aactaattga tgttggtggg ttggagaata aggagtacaa taagttgttt 1020
 313 tgggctgtgc atccagggtg gcctgcgata ttgaatcgcg tggagaagcg gcttgagttg 1080
 316 tcgccgcaga agctgaatgc tagtagaaaa gctctaattg attatggaaa tgctagcagc 1140
 319 aatactattg tttatgtgct ggaatatatg ctagaagagg aaaagaagat taaaaaggcg 1200
 322 ggtggaggag attctgaatg gggattgata cttgcttttg gacctggaat tacttttgag 1260
 325 gggattctag caaggaactt gtgtgcatga agtcttatac aattgtgatg catgacttat 1320
 328 actcttattt ctactaatta ttatattaag caaattcaga acttttaagt aatgatttaa 1380
 331 tgaagaatac ttatagtata ttgactttat tcaacttcaa agcaagttaa tgatcctaag 1440
 334 acatggtaga acttgagcat gtggaatagt tgtaacaaaa actctaagca aatagagact 1500
 337 ttatgtagta taaagcattt ccagacatga taaataatgg tacctcagaa cataaaatat 1560
 340 atttagctat ctttcatccc caactttaca catccaccaa ggtacagaat aagcatatgt 1620
 343 caacacaaaa tgtactctaa gtctaacaat agtaacacaa catgatgcct gattaagtta 1680
 346 aaagaaaaga aaatctgagg gcatagatct tcaatcacac cactccagag ggaaggcgta 1740
 349 gaacaagctg tccgccgaaa aacttgcaat tcaataaata tcattaggac aacagtgcag 1800

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352 agtcatgcgg gaaatgtctt aagtcactgt actaaaaata taggattata ttatgaacta 1860
355 tactaacctt ttcacataat agtaacagaa atcagctaag atgaatgtct ggacaatttc 1920
358 tgagataaga accatgacgg ccataagcca taccccaagg caaccaataa atgtccacgg 1980
361 gtatctaaca cctgttgcaa gaaatagtaa gttattagga gatgtgcggt tacgaaattc 2040
364 aagctacaca acaaaaggag gccagaacaa cagcaatctt gtaaccagat gacaacaata 2100
367 aaatgtaaac ttaaagagac cgaacacaca aacattgcaa ctcagatgga attgctgcca 2160
370 tgtaactagt aggagatttg ggacgtcaaa tcagtattt atgcaaatac aaggatatgac 2220
373 cgccttgtct attgtagcat acaacaaacg tacagtgggt ttgtccctct caaaatggca 2280
376 ggatctttac agcacaatat ttggttttgt catacttata ccataaaaaa aaaaaaaaaa 2340
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383 <210> SEQ ID NO: 4
384 <211> LENGTH: 391
385 <212> TYPE: PRT
386 <213> ORGANISM: Trifolium repens
389 <400> SEQUENCE: 4
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397 Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu
398 20 25 30
402 Val Met Gln Glu Cys Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys
403 35 40 45
407 Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
408 50 55 60
412 Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
413 65 70 75 80
417 Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
418 85 90 95
422 Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
423 100 105 110
427 Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
428 115 120 125
432 Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
433 130 135 140
437 Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
438 145 150 155 160
442 Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
443 165 170 175
447 Asp Val Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
448 180 185 190
452 Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
453 195 200 205
457 Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
458 210 215 220
462 Ile Gly Ser Asp Pro Val Phe Glu Thr Glu Thr Pro Leu Phe Glu Leu
463 225 230 235 240
467 His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
468 245 250 255
472 Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
473 260 265 270

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477 Pro Gln Ile Ile Glu Asp Asn Val Glu Gly Phe Cys Asn Lys Leu Ile
478          275          280          285
482 Asp Val Val Gly Leu Glu Asn Lys Glu Tyr Asn Lys Leu Phe Trp Ala
483      290          295          300
487 Val His Pro Gly Gly Pro Ala Ile Leu Asn Arg Val Glu Lys Arg Leu
488 305          310          315          320
492 Glu Leu Ser Pro Gln Lys Leu Asn Ala Ser Arg Lys Ala Leu Met Asp
493          325          330          335
497 Tyr Gly Asn Ala Ser Ser Asn Thr Ile Val Tyr Val Leu Glu Tyr Met
498          340          345          350
502 Leu Glu Glu Glu Lys Lys Ile Lys Lys Ala Gly Gly Gly Asp Ser Glu
503          355          360          365
507 Trp Gly Leu Ile Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Ile
508      370          375          380
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513 385          390
517 <210> SEQ ID NO: 5
518 <211> LENGTH: 1653
519 <212> TYPE: DNA
520 <213> ORGANISM: Trifolium repens
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530 gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgctcc tactcagga      180
533 aaggcaacga tacttgcatc aggaaaggct ttccccgccc aggtcctccc tcaagagtgc      240
536 ttggtggaag gattcattcg cgacactaag tgtgacgata cttatattaa ggagaaattg      300
539 gagcgtcttt gcaaaaacac aactgtgaaa acaagataca cagtaatgtc aaaggagatc      360
542 ttagacaact atccagagct agccatagat ggaacaccaa caataaggca aaagcttgaa      420
545 atagcaaatc cagcagtagt tgaaatggca acaagagcaa gcaaagattg catcaaagaa      480
548 tggggaaggt cacctcaaga tatcacacac atagtctatg tttcctcgag cgaaattcgt      540
551 ctaccgggtg gtgaccttta tcttgcaaat gaactcggtt taaacagcga tgtaaatcgc      600
554 gtaatgctct atttctctcg ttgctacggc ggtgtcactg gcttacgtgt cgccaaagac      660
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575 gacttatattt gggctgttca tcctggtggg ccagctatac tcaataagct agaaaatata      1080
578 ctcaaatgaa aaagtgataa attggattgt agtaggaagg cattaatgga ttatggaaat      1140
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587 ctctccgta gcctttaatc ttgaaataat aattcatatg aaattacttg tcttaagatt      1320
590 gtgataggaa gatgaatatg tattggatta atattgatat ggtgttattt taagttgatt      1380
593 ttaaaaaaag tttattaata aagtatgatg taacaattgt tgtttgaatg ttaaaagggg      1440
596 agtatactat tttaagttct tgaccatact gattttttct ttacacattt tcatatctaa      1500
599 aattgttcta tgatatcttc attgttgata ctgtaataat ataatatcta atttggctgg      1560
602 caaatgaaa gatttttcac cgaaaaaaa aaaaaaaaa aaaaaaaaa aagtactctg      1620
605 cgttgttacc actgcttaac cactagtga ttc      1653

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Input Set : A:\sequence.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40

Seq#:41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64

Seq#:65,66,67,68,69,70,71,72,73,74,75,76,77

VERIFICATION SUMMARY

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L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD